

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Hauptmann, R.  
Falkner, E.  
Bodo, G.  
Voß, T.  
Maurer-Fogy, I.
- (ii) TITLE OF INVENTION: Process for Preparing and Purifying  
alpha-Interferon
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
(B) STREET: 1100 New York Avenue, Suite 600  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: U.S.A.  
(F) ZIP: 20005
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/249,671  
(B) FILING DATE: 26-MAY-1994  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0652.1350000
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202) 371-2600  
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTCTTCAAG AATTCGAGAT TATCG

25

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC 56

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGCCTATGC ATGTGATCTG CCTCAAACCC ACAGC 35

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGCAGATCAC ATGCATAGGC ATTTGTAGCA ATAG 34

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 165 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30

1  
B  
cont.

29

Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
145 150 155 160

Leu Arg Ser Lys Glu  
165

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 495 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG AGG ACC TTG ATG  
48  
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15

CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC  
96  
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30

AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC AAC CAG TTC CAA  
144  
Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45

AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC  
192

B1  
Cont.

30

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60

AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG GAT GAG ACC CTC  
240

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80

CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA  
288

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95

GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG  
336

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
100 105 110

GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC  
384

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
115 120 125

TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA  
432

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
130 135 140

GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT  
480

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
145 150 155 160

TTA AGA AGT AAG GAA  
495

Leu Arg Ser Lys Glu  
165

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG  
60

TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC  
120

GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA  
180

31  
Cont.

31

AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTACACGG CCGAGACTTA TAGTCGCTTT  
240

GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTTATGAA AAAGAATATC  
300

GCATTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAATGCCTA TGCATGTGAT  
360

CTGCCCTCAA CCCACAGCCT GGGTAGCAGG AGGACCTTGA TGCTCCTGGC ACAGATGAGG  
420

AGAATCTCTC TTTTCTCCTG CTTGAAGGAC AGACGTGACT TTGGATTTCC CCAGGAGGAG  
480

TTTGGCAACC AGTTCCAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT GATCCAGCAG  
540

ATCTTCAATC TCTTCAGCAC AAAGGACTCA TCTGCTGCTT GGGATGAGAC CCTCCTAGAC  
600

AAATTCTACA CTGAACTCTA CCAGCAGCTG AATGACCTGG AAGCCTGTGT GATACAGGGG  
660

GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT GAGGAAATAC  
720

TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC CTGGGAGGTT  
780

GTCAGAGCAG AAATCATGAG ATCTTTTTTCT TTGTCAACAA ACTTGCAAGA AAGTTTAAGA  
840

AGTAAGGAAT GATAACGATC GTAACGTGCA  
869

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 286..873
- (D) OTHER INFORMATION: /function= "Cytokine"  
/product= "Interferon-omegal"

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 355..873
- (D) OTHER INFORMATION: /function= "Cytokine"  
/product= "Interferon-omega"

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 286..354
- (D) OTHER INFORMATION: /product= "ST II Leader"

31  
Cont.

32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAATTGGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA CCAACAGCGG  
60

TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC  
120

GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA  
180

AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT  
240

GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG  
294

Met Lys Lys  
-23

AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA  
342

Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr  
-20 -15 -10 -5

AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG  
390

Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg  
1 5 10

AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG  
438

Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu  
15 20 25

TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA  
486

Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys  
30 35 40

GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG  
534

Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met  
45 50 55 60

CTG CAG CAG ATC TTC AGC CTC TTC CAC ACA GAG CGC TCC TCT GCT GCC  
582

Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala  
65 70 75

TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA  
630

Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln  
80 85 90

CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA  
678

Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu  
95 100 105

TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC  
726

Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe  
110 115 120

B1  
Cont

33

CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC  
774  
Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala  
125 130 135 140

TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA  
822  
Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr  
145 150 155

AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT  
870  
Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser  
160 165 170

TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC TCTGGTCAAT  
930

TCAAAAGACT CTTATTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC TGCAAATACT  
990

TTGTCGGTAT ATTAAGCCAG TATATGTAA AAAGACTTAG GTTCAGGGGC ATCAGTCCCT  
1050

AAGATGTTAT TTATTTTAC TCATTTATTT ATTCTTACAT TTTATCATAT TTATACTATT  
1110

TATATTCTTA TATAACAAAT GTTTGCCTTT ACATTGTATT AAGATAACAA AACATGTTCA  
1170

GGATCCA  
1177

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser  
-23 -20 -15 -10

Ile Ala Thr Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu  
-5 1 5

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
10 15 20 25

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
30 35 40

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
45 50 55

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
60 65 70

B1  
cont.

34

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
75 80 85  
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
90 95 100 105  
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
110 115 120  
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
125 130 135  
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
140 145 150  
Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
155 160 165  
Gly Ser Ser  
170

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 879 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 286..852

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 355..852
- (D) OTHER INFORMATION: /function= "Cytokine"  
/product= "Interferon-alpha-2c"

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 286..354
- (D) OTHER INFORMATION: /product= "ST II Leader"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAATGA CCAACAGCGG  
60

TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG CATTCCTGAC  
120

GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA  
180

AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA TAGTCGCTTT  
240

B<sup>1</sup>  
cont.

35



GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTT ATG AAA AAG  
294

Met Lys Lys  
-23

AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA  
342

Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr  
-20 -15 -10 -5

AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG  
390

Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg  
1 5 10

AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC  
438

Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser  
15 20 25

TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC  
486

Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly  
30 35 40

AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC  
534

Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile  
45 50 55 60

CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG  
582

Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp  
65 70 75

GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG  
630

Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu  
80 85 90

AAT GAC CTG GAA GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT  
678

Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr  
95 100 105

CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA  
726

Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln  
110 115 120

AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG  
774

Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp  
125 130 135 140

GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC  
822

Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn  
145 150 155

B1  
cont.

TTG CAA GAA AGT TTA AGA AGT AAG GAA TGATAACGAT CGTAACTGCA  
 869  
 Leu Gln Glu Ser Leu Arg Ser Lys Glu  
 160 165

GAAGCTTAAT  
 879

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 188 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser  
 -23 -20 -15 -10  
 Ile Ala Thr Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu  
 -5 1 5  
 Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser  
 10 15 20 25  
 Leu Phe Ser Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu  
 30 35 40  
 Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His  
 45 50 55  
 Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser  
 60 65 70  
 Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr  
 75 80 85  
 Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
 90 95 100 105  
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys  
 110 115 120  
 Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro  
 125 130 135  
 Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu  
 140 145 150  
 Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu  
 155 160 165

B<sup>1</sup>  
 cont.